

AMENDMENTS TO THE CLAIMS:

Claims 1-24 are canceled without prejudice or disclaimer. Claims 25-58 are added. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-24 (Cancelled.)

Claim 25. (New.) A variant of a parent alpha-amylase, comprising an alteration selected from the group of alterations corresponding to R118K, R320K or R458K (using SEQ ID NO:12 for numbering), wherein the variant has alpha-amylase activity, and wherein the variant has at least 80% homology to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12 and SEQ ID NO:13.

Claim 26. (New.) The variant of claim 25, comprising an alteration corresponding to R118K.

Claim 27. (New.) The variant of claim 25, comprising an alteration corresponding to R320K.

Claim 28. (New.) The variant of claim 25, comprising an alteration corresponding to R458K.

Claim 29. (New.) The variant of claim 25, comprising an alteration corresponding to R118K, R320K and R458K.

Claim 30. (New.) The variant of claim 25, wherein the parent alpha-amylase is selected from the group consisting of *B. licheniformis* alpha-amylase, *B. stearothermophilus* alpha-amylase, *B. amyloliquefaciens* alpha-amylase, *Bacillus sp.* NCIB 12289 alpha-amylase, *Bacillus sp.* NCIB 12512 alpha-amylase, *Bacillus sp.* NCIB 12513 alpha-amylase, *Bacillus sp.* DSM 9357 alpha-amylase, *Bacillus sp.* DSMZ no. 12649 alpha-amylase, *Bacillus sp.* KSM AP1378 alpha-amylase, *Bacillus sp.* KSM K36 alpha-amylase and *Bacillus sp.* KSM K38 alpha-amylase.

Claim 31. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of SEQ ID NO:2.

Claim 32. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of SEQ ID NO:2.

Claim 33. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of SEQ ID NO:6.

Claim 34. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of SEQ ID NO:8.

Claim 35. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of SEQ ID NO:10.

Claim 36. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of SEQ ID NO:12.

Claim 37. (New.) The variant of claim 25, wherein the variant has at least 80% homology with an amino acid sequence of and SEQ ID NO:13.

Claim 38. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of SEQ ID NO:2.

Claim 39. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of SEQ ID NO:2.

Claim 40. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of SEQ ID NO:6.

Claim 41. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of SEQ ID NO:8.

Claim 42. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of SEQ ID NO:10.

Claim 43. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of SEQ ID NO:12.

Claim 44. (New.) The variant of claim 25, wherein the variant has at least 90% homology with an amino acid sequence of and SEQ ID NO:13.

Claim 45. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of SEQ ID NO:2.

Claim 46. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of SEQ ID NO:2.

Claim 47. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of SEQ ID NO:6.

Claim 48. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of SEQ ID NO:8.

Claim 49. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of SEQ ID NO:10.

Claim 50. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of SEQ ID NO:12.

Claim 51. (New.) The variant of claim 25, wherein the variant has at least 95% homology with an amino acid sequence of and SEQ ID NO:13.

Claim 52. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of SEQ ID NO:2.

Claim 53. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of SEQ ID NO:2.

Claim 54. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of SEQ ID NO:6.

Claim 55. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of SEQ ID NO:8.

Claim 56. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of SEQ ID NO:10.

Claim 57. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of SEQ ID NO:12.

Claim 58. (New.) The variant of claim 25, wherein the variant has at least 97% homology with an amino acid sequence of and SEQ ID NO:13.